

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WASTFALT, Maria K. Boden
FLOCK, Jan-Ingmar
- (ii) TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
(B) STREET: P.O. Box 1404
(C) CITY: Alexandria
(D) STATE: Virginia
(E) COUNTRY: United States
(F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TBA (Div of US 09/276,141)
(B) FILING DATE: Even date herewith
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/276,141
(B) FILING DATE: 25-03-99
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/244,229
(B) FILING DATE: 09-DEC-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: SE 9202720-0
(B) FILING DATE: 21-SEP-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: SE 9302955-1
(B) FILING DATE: 13-SEP-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/SE93/00759
(B) FILING DATE: 20-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: McGowan, Malcolm K.

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(B) REGISTRATION NUMBER: 39,300
(C) REFERENCE/DOCKET NUMBER: 012889-011

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (703) 836-6620
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Asn Ser
1 5 10 15

Lys Tyr Gly Thr
 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Lys Ser
1 5 10 15

Lys Lys Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
1 5 10 15
Lys Asn Gly Thr
20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
1 5 10 15
Lys Asn Gly Thr
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
1 5 10 15
Asn Ile Val Glu
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Tyr Pro Glu Lys Lys Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCGAAGGA TACGGTCCAA GAGAAAAGAA ACCAGTGAGT ATTAATCACA ATATCGTAGA	60
GTACAATGAT GGTACTTTTA AATATCAATC TAGACCAAAA TTAACTCAA CACCTAAATA	120
TATTAAATTC AAACATGACT ATAATATTTT AGAATTTAAC GATGGTACAT TCGAATATGG	180
TGCACGTCCA CAATTTAATA AACCAGCAGC GAAAACGTGAT GCAACTATTA AAAAGAACA	240
AAAATTGATT CAAGCTCAAA ATCTTGTGAG AGAATTTGAA AAAACACATA CTGTCAGTGC	300
ACACAGAAAA GCACAAAAGG CAGTCAACTT AGTTTCGTTT GAATACAAAG TGAAGAAAAT	360
GGTCTTACAA GAGCGAATTG ATAATGTATT AAAACAAGGA TTAGTGAG	408

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His	
1 5 10 15	
Asn Ile Val Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro	
20 25 30	
Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn	
35 40 45	

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Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln
50 55 60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln
65 70 75 80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His
85 90 95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser
100 105 110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn
115 120 125

Val Leu Lys Gln Gly Leu Val Arg
130 135

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1009 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 157..654

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 804..1007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTAGTGTA TAAGTGCTGA TGAGTCACAA GATAGATAAC TATATTTTGT CTATATTATA 60

AAGTGTTTAT AGTTAATTAA TAATTAGTTA ATTTCAAAAG TTGTATAAAT AGGATAACTT 120

AATAAATGTA AGATAATAAT TTGGAGGATA ATTAAC ATG AAA AAT AAA TTG ATA 174
Met Lys Asn Lys Leu Ile
1 5

GCA AAA TCT TTA TTA ACA ATA GCG GCA ATT GGT ATT ACT ACA ACT ACA 222
Ala Lys Ser Leu Leu Thr Ile Ala Ala Ile Gly Ile Thr Thr Thr Thr
10 15 20

ATT GCG TCA ACA GCA GAT GCG AGC GAA GGA TAC GGT CCA AGA GAA AAG 270
Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro Arg Glu Lys
25 30 35

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AAA CCA GTG AGT ATT AAT CAC AAT ATC GTA GAG TAC AAT GAT GGT ACT	318
Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn Asp Gly Thr	
40 45 50	
TTT AAA TAT CAA TCT AGA CCA AAA TTT AAC TCA ACA CCT AAA TAT ATT	366
Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro Lys Tyr Ile	
55 60 65 70	
AAA TTC AAA CAT GAC TAT AAT ATT TTA GAA TTT AAC GAT GGT ACA TTC	414
Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp Gly Thr Phe	
75 80 85	
GAA TAT GGT GCA CGT CCA CAA TTT AAT AAA CCA GCA GCG AAA ACT GAT	462
Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala Lys Thr Asp	
90 95 100	
GCA ACT ATT AAA AAA GAA CAA AAA TTG ATT CAA GCT CAA AAT CTT GTG	510
Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln Asn Leu Val	
105 110 115	
AGA GAA TTT GAA AAA ACA CAT ACT GTC AGT GCA CAC AGA AAA GCA CAA	558
Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg Lys Ala Gln	
120 125 130	
AAG GCA GTC AAC TTA GTT TCG TTT GAA TAC AAA GTG AAG AAA ATG GTC	606
Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys Lys Met Val	
135 140 145 150	
TTA CAA GAG CGA ATT GAT AAT GTA TTA AAA CAA GGA TTA GTG AGA TAA	654
Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu Val Arg *	
155 160 165	
TACTTCTGTC ATTATTTTAA GTTCAAAATA ATTTAATATT ATATTATTTT TTATTAATAA	714
AACGACTATG CTATTTAATG CCAGGTTAAT GTAACCTTCC TAAAATTGAC TATATAATCG	774
TTAAGTATCA ATTTTAAGGA GAGTTTACA ATG AAA TTT AAA AAA TAT ATA TTA	827
Met Lys Phe Lys Lys Tyr Ile Leu	
1 5	
ACA GGA ACA TTA GCA TTA CTT TTA TCA TCA ACT GGG ATA GCA ACT ATA	875
Thr Gly Thr Leu Ala Leu Leu Ser Ser Thr Gly Ile Ala Thr Ile	
10 15 20	
GAA GGG AAT AAA GCA GAT GCA AGT AGT CTG GAC AAA TAT TTA ACT GAA	923
Glu Gly Asn Lys Ala Asp Ala Ser Ser Leu Asp Lys Tyr Leu Thr Glu	
25 30 35 40	
AGT CAG TTT CAT GAT AAA CGC ATA GCA GAA GAA TTA AGA ACT TTA CTT	971
Ser Gln Phe His Asp Lys Arg Ile Ala Glu Glu Leu Arg Thr Leu Leu	
45 50 55	

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AAC AAA TCG AAT GTA TAT GCA TTA GCT GCA GGA AGC TT	1009
Asn Lys Ser Asn Val Tyr Ala Leu Ala Ala Gly Ser	
60 65	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAGATAACT ATATTTTGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA	60
TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA	120
TTAACATGAA AAATAAATTG ATAGCAAAAT CTTTATTAAC AATAGCGGCA ATTGGTATTA	180
CTACAACTAC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA	240
AACCAAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT	300
CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT	360
TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG	420
CGAAACTGA TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA	480
GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT	540
TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT	600
TAAACAAGG ATTAGTGAGA TAATACTTCT GTCATTATTT TAAGTTCAAA ATAATTTAAT	660
ATTATATTAT TTTTATTAA TAAACGACT ATGCTATTTA ATGCCAGGTT AATGTAACTT	720
TCCTAAAATT GACTATATAA TCGTTAAGTA TCAATTTTAA GGAGAGTTTA CAATGAAATT	780
T	781

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAGATAGCT ATATTTCAGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA 60
TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA 120
TTGACATGAA AAATGCATTG ATAGCAAAAT CTTTATTAAC ATTAGCGGCA ATAGGTATTA 180
CTACAACTAC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA 240
AACCAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT 300
CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT 360
TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG 420
CGAAAACCTGA TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA 480
GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT 540
TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT 600
TAAAACAAGG ATTAGTTAAA TAAAACTTCA ATCGTTGCTG TTATCTGGAA ATAATTAATT 660
AAATGTTATG TTAATTTTTG TTAATGAAAA AAGTAATCTA TTTAATGACA GGTTAATGTA 720
ATTGTCCTGA AATTGACTAT ATACTCAGTA AGTATCAATT TTAAGGAGAG CTTATAATGA 780
AATT 785

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Asn Lys Leu Ile Ala Lys Ser Leu Leu Thr Ile Ala Ala Ile
1 5 10 15
Gly Ile Thr Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly
20 25 30
Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val
35 40 45

Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn
50 55 60

Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu
65 70 75 80

Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys
85 90 95

Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile
100 105 110

Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser
115 120 125

Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr
130 135 140

Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys
145 150 155 160

Gln Gly Leu Val Arg
165

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Lys Asn Ala Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile
1 5 10 15

Gly Ile Thr Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly
20 25 30

Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val
35 40 45

Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn
50 55 60

Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu
65 70 75 80

Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys
85 90 95

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Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile
 100 105 110

Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser
 115 120 125

Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr
 130 135 140

Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys
 145 150 155 160

Gln Gly Leu Val Lys
 165

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
 1 5 10 15

Asn Ile Val Glu Tyr Asn Asp Gly Ser Phe Lys Tyr Gln Ser Arg Pro
 20 25 30

Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn
 35 40 45

Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln
 50 55 60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln
 65 70 75 80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His
 85 90 95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser
 100 105 110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn
 115 120 125

Val Leu Lys Gln Gly Leu Val Arg
 130 135

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala	Ser	Gln	Tyr	Gly	Pro	Arg	Pro	Gln	Phe	Asn	Lys	Thr	Pro	Lys	Tyr	1	5	10	15
Val	Lys	Tyr	Arg	Asp	Ala	Gly	Thr	Gly	Ile	Arg	Glu	Tyr	Asn	Asp	Gly	20	25	30	
Thr	Phe	Gly	Tyr	Glu	Ala	Arg	Pro	Arg	Phe	Asn	Lys	Pro	Ser	Glu	Thr	35	40	45	
Asn	Ala	Tyr	Asn	Val	Thr	Thr	His	Ala	Asn	Gly	Gln	Val	Ser	Tyr	Gly	50	55	60	
Ala	Arg	Pro	Thr	Tyr	Lys	Lys	Pro	Ser	Glu	Thr	Asn	Ala	Tyr	Asn	Val	65	70	75	80
Thr	Thr	His	Ala	Asn	Gly	Gln	Val	Ser	Tyr	Gly	Ala	Arg	Pro	Thr	Gln	85	90	95	
Asn	Lys	Pro	Ser	Glu	Thr	Asn	Ala	Tyr	Asn	Val	Thr	Thr	His	Gly	Asn	100	105	110	
Gly	Gln	Val	Ser	Tyr	Gly	Ala	Arg	Gln	Ala	Gln	Asn	Lys	Pro	Ser	Lys	115	120	125	
Thr	Asn	Ala	Tyr	Asn	Val	Thr	Thr	His	Ala	Asn	Gly	Gln	Val	Ser	Tyr	130	135	140	
Gly	Ala	Arg	Pro	Thr	Tyr	Lys	Lys	Pro	Ser	Lys	Thr	Asn	Ala	Tyr	Asn	145	150	155	160
Val	Thr	Thr	His	Ala	Asp	Gly	Thr	Ala	Thr	Tyr	Gly	Pro	Arg	Val	Thr	165	170	175	
Lys																			

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